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Publication date:
2013

THE INTESTINAL MICROBIOTA IN RAINBOW TROUT (*ONCORHYNCHUS MYKISS*) IS INFLUENCED BY DIET TYPE AND *YERSINIA RUCKERI* CHALLENGE

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In recent years it has become more and more evident that the bacterial flora in the gut of warm-blooded animals modulates physiological processes and the immunological status of the host. Besides effects on growth parameters, commensal intestinal bacteria balance the immune system and prevent colonization of pathogenic bacteria. The question is if the gut microbiota is also important in lower vertebrates such as fish? Is the microbiota related to the diet type and does it play a protective role in connection to pathogenic challenge? To examine these questions rainbow trout fry were fed two different diets of either a marine or vegetable origin from first feeding and onwards. At a size of about four gram the fish were bath challenged by *Yersinia ruckeri* serotype O1 and intestines were then sampled 5 days post challenge for subsequent metagenomic examination. Next-generation sequencing was applied for the metagenomic studies using the Illumina HiSeq 2000 platform. The results showed two distinctly different microbial patterns in the intestines dependent on the diet type. Fish fed a marine based diet overall had a significantly higher amount of the class β-proteobacteria, while the amount of reads belonging to phylum Firmicutes were significantly higher in the intestines of vegetable fed fish. The genera within phylum Firmicutes present in significantly higher amounts in vegetable fed fish were *Weissella*, *Leuconostoc* and *Streptococcus*. Genus *Aeromonas* from the γ-proteobacteria class was also present in significantly higher amounts in the vegetable fed fish. When challenged with *Yersinia ruckeri*, fish with a high amount of sequence reads belonging to genus *Yersinia* had a significantly lower amount of reads from the order Burkholderiales relative to non-infected control fish and fish with a low amount of *Yersinia* specific sequences. Further, these infected fish further clustered separately when analyzing the bacterial community on a PCA plot. The immunological examinations using RT-qPCR showed similar constitutive expression between the two diet groups, but the response differed between the two diet groups in challenged fish. Here, the general pattern was a pro-inflammatory response in the intestine of marine fed fish challenged with *Yersinia ruckeri* relative to non-infected control fish, while several immune genes were down-regulated in vegetable fed fish relative to non-infected control fish. Overall, the results indicate that the gut microbiota in rainbow trout is highly plastic according to the type of diet and does further seem to be involved in the immunological response in connection to pathogenic challenge.